

# PROGRAM ACTIVITY REPORT (PAR)



## UPDATE ON U.S. FERAL SWINE GENETICS

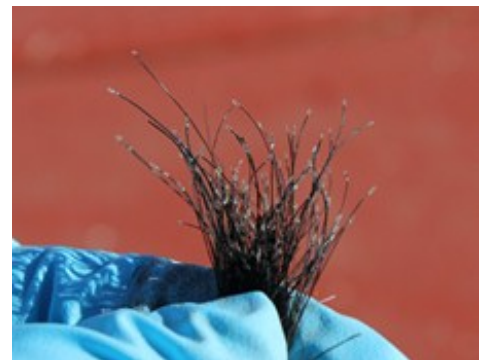
Feral swine represent an important reservoir for a number of diseases that could be introduced into commercial production swine populations. Feral swine disease and population management would benefit from a better understanding of the types of pigs constituting populations throughout the U.S. For example, research suggests that hybrid Eurasian wild boar (EWB) are more capable invaders than feral domestic pigs. Hence, where hybrids are detected, we might predict rapid range expansion or greater competitive interaction with native species. Also, domestic breeds and EWB vary in behavior, fecundity and other life-history traits potentially important for survival and population-level response to disease or control efforts. Research has also shown that EWB and hybrids may be more resistant to certain diseases than are feral swine derived solely from domestic breeds.



Knowledge of the genetic ancestry of feral swine across the U.S. would prove useful in predicting relative disease risk across different populations and would allow fine tuning of population and disease management efforts.

Molecular techniques can provide insights on origins of feral swine populations useful for management. Recent advances in whole genome sequencing have led to the discovery of thousands of Single Nucleotide Polymorphisms (SNPS) within the swine genome that have enabled a number of new genetic analytic approaches to be utilized, including comparative genetic studies, identification of quantitative traits linked to disease resistance, and characterization of genotypic variation that may be useful for a number of unforeseen management purposes. Analyses may allow differentiation of a number of unique SNPs associated with disease resistance, favorable/unfavorable life history traits, and ancestry related to EWB, hybrid, and domestic individuals at the sounder and local population level scales. The same SNP information is also relevant for population level genetic profiles at multi-county, state, and national scales to help guide comprehensive disease and population management decisions related to feral swine.

The NWDP, in collaboration with the National Park Service and the Univer-



sity of North Dakota, have begun analyzing a dataset of 950+ individuals consisting mainly of Wildlife Services collected feral swine (n=870) from 32 states. Individuals were tested using either a 60K SNP assay or a 96 SNP assay. A small number of pure EWB and domestic swine were included in the dataset for reference. This information should prove useful in future management activities including disease risk assessment and abatement, characterization of past and future translocation events, and feral swine population structure assessments.

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*The original artwork on this page was created by the National Wildlife Disease Program's Erika Kampe and Sarah Goff*



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